Institut für Lebensmittelsicherheit und -hygiene
der Vetsuisse-Fakultät Universität Zürich

Direktor: Prof. Dr. Roger Stephan

Arbeit unter wissenschaftlicher Betreuung von
Dr. Sophia Johler

Staphylococcus aureus isolated from colostrum of dairy heifers represent a closely related group exhibiting highly homogeneous genomic and antimicrobial resistance features

Inaugural-Dissertation

zur Erlangung der Doktorwürde der
Vetsuisse-Fakultät Universität Zürich

vorgelegt von

Ueli Stalder

Tierarzt
von Schüpfheim/LU

genehmigt auf Antrag von

Prof. Dr. Roger Stephan, Referent

2014

Contents

Abstract

In heifers, intramammary infections caused by *Staphylococcus (Staph.) aureus* affect milk production and udder health in the first and subsequent lactations, and can lead to premature culling. Not much is known about *S. aureus* isolated from heifers and it is also unclear whether or not these strains are readily transmitted between heifers and lactating herd mates. In this study, we compare phenotypic characteristics, *spa* types, and DNA microarray virulence and resistance gene profiles of *Staph. aureus* isolates obtained from colostrum samples of dairy heifers to isolates obtained from lactating cows. Our objective was to (I) characterize *Staph. aureus* strains associated with mastitis in heifers, and (II) determine relatedness of *Staph. aureus* strains from heifers and lactating cows in order to provide data on transmission. We analyzed colostrum samples of 501 heifers and milk samples of 68 lactating cows within the same herd, isolating 48 and nine *Staph. aureus* isolates, respectively. *Staph. aureus* strains from heifers, lactating herd mates, and an unrelated collection of 78 strains from bovine mastitis milk of mature cows were compared. With one exception each, characterization of all strains from heifers and lactating cows in the same herd yielded highly similar phenotypic and genotypic results. The strains were SLAT(-), belonged to *agr* type II, CC705, and *spa* types t529 and t12926. They were susceptible to all antimicrobial agents tested. In contrast, the strains from mature cows in other herds were spread across different clonal complexes, *spa* types, and SplitsTree clusters, thus displaying a far higher degree of heterogeneity. We conclude that strains isolated from colostrum of heifers and mastitis milk of lactating cows in the same herd feature highly similar phenotypic and genomic characteristics, suggesting persistence of the organism during the first and potentially subsequent lactations or transmission between heifers and mature herd mates.

Key words: *Staphylococcus aureus*, dairy heifer, bovine mastitis, genotyping

Introduction

Heifer mastitis leads to considerable financial losses in the dairy industry, as it affects not only future milk performance and udder health, but also leads to premature culling (Compton et al., 2007; Piepers et al., 2010). To date, it is still poorly understood, which sources of infection and routes of transmission play a role in *Staph. aureus* mastitis in heifers. Heifers have never been milked and were thus not exposed to the milking process and vacuum, which represent major risk factors for contagious mastitis in lactating cows. However, *Staph. aureus* can be detected in milk samples of up to 15% of heifers prepartum and in up to 8% of heifers at first parturition (Fox, 2009). While heifers were suggested to represent a reservoir of *Staph. aureus* to uninfected herd mates (Roberson et al., 1994), another study suggested that the udder of lactating cows might be an infection source of contagious major pathogens for heifers (Piepers et al., 2011). In a recent review, De Vliegher et al. summarize the controversial discussion on transmission of *Staph. aureus* between heifers and mature cows and declare the need for further studies using strain typing (De Vliegher et al., 2012).

In this study, we compare DNA microarray profiles and *spa* types, as well as phenotypic characteristics of *Staph. aureus* isolates obtained from colostrum samples of dairy heifers to isolates obtained from mastitis milk of lactating cows. Our objective was to (I) characterize *Staph. aureus* strains associated with mastitis in heifers, and (II) determine relatedness of *Staph. aureus* strains from heifers and lactating herd mates in order to provide data on transmission.

Materials and Methods

Colostrum samples of 501 heifers form a randomized selection of 72 farms in Switzerland were collected. Sampling was performed within 24 hours post partum. In addition, a total of 68 samples from lactating cows within the same herd including first lactation animals were

taken on seven farms, which harbored heifers that had been tested positive for *Staph. aureus*. Only milk from lactating cows with clinical signs of mastitis or milk that had been tested positive in the California mastitis test was collected. For all tested cows, quarter milk samples were collected by the farmers. We compared strains from heifers (H) and lactating cows within the same herd (LC) to strains from an unrelated collection (C) of 78 *Staph. aureus* strains that were used in a comprehensive study investigating bovine mastitis isolates from mature cows in Switzerland (Moser et al., 2013).

We characterized the strains using latex agglutination test, antimicrobial susceptibility testing, *spa* typing, and a DNA microarray. Staphaurex latex agglutination test (SLAT) was performed using the Staphaureux Plus kit (Oxoid, Basel, Switzerland) according to the manufacturer's instructions. For susceptibility testing, the following agents were tested: ampicillin (10 μg), amoxicillin (20 μg) with clavulanic acid (10 μg), cephalothin (30 μg), ceftiofur (30 μg), erythromycin (15 μg), cefoxitin (30 μg), gentamicin (10 μg), kanamycin (30 μg), cefalexin-kanamycin (15 μg - 30 μg), penicillin (10 IU), and penicillin-novobiocin (10 IU - 30 μg). Disks containing cefalexin-kanamycin (Ubrolexin) were provided by Boehringer Ingelheim (Basel, Switzerland), disks containing ceftiofur, penicillin and penicillin-novobicin were obtained from Oxoid (Basel, Switzerland), and all other disks were provided by Becton Dickinson (Basel, Switzerland). Disk diffusion was performed on Mueller-Hinton agar and *Staph. aureus* ATCC 25923 was used as a quality control. Strains were classified according to Clinical and Laboratory Standards Institute standard protocols (CLSI, 2008), except for cefalexin-kanamycin, for which preliminary interpretive breakpoints recommended by Pillar were used (Pillar et. al., 2009). *Spa* types were determined as previously described (Wattinger et al., 2012). For the DNA microarray assay, we used the *Staph. aureus* Genotyping Kit (Alere Technologies GmbH, Jena, Germany) to detect the absence or presence of 333 genes and their allelic variants and to assign strains to clonal complexes. Microarray data from a

comprehensive study by Moser et al. (Moser et al., 2013) on characteristic features of *Staph. aureus* isolated from mastitis milk of lactating cows (C) in Switzerland served as a control to assess unique features among the virulence and resistance genes of *Staph. aureus* strains isolated from heifers (H) and from lactating cows in the same herd (LC). For statistical analysis, the distribution of genes was compared based on DNA microarray results using SPSS Statistics 21 (SPSS Inc., Chicago, IL) to run the Pearson χ^2 test to identify significant associations between the source of the strains and the presence of the genes. Fisher's Exact test was used in case the expected count was less than five. Results were considered statistically significant for *P*-values <0.05.

Results

We isolated *Staph. aureus* from 10% of heifer colostrum samples and 13% of LC mastitis milk samples. Isolates exhibiting identical microarray patterns, as well as identical CC and *spa* type assignments were considered to represent the same strain (Supplement 1). Six heifer strains were isolated in duplicate (H_5, H_6, H_7, H_8, H_15, H_22), one LC strain in triplicate (LC_7), and two strains could be found among both heifers and lactating herd mates (H_15 = LC_2, H_22 = LC_1). Five of the six strains that were isolated in duplicate among heifers, were isolated at farm A, as well as from at least one heifer or lactating cow in another farm (farms B/C/D/E). Interestingly, an additional seven H strains (H_16-H_21, H_29) were isolated on farm A.

With one exception each, characterization of all strains from heifers and lactating cows in the same herd yielded highly similar phenotypic and genotypic results. The strains were SLAT(-), belonged to *agr* type II, CC705, and *spa* types t529 (n = 38) and t12926 (n = 1). They were also susceptible to all antimicrobial agents tested in the disk diffusion assay. In addition, this group of strains formed a highly homogeneous subcluster within the CC705 cluster of the

SplitsTree (Supplement 2), exclusively comprising H and LC strains. In contrast, the C strains were spread across different clonal complexes and SplitsTree clusters, thus displaying a far higher degree of heterogeneity. Only H_14 and LC_7 were not integrated into the highly homogeneous group and exhibited a SLAT(+) phenotype, as well as differing clonal complexes and *spa* types (H_14: CC97, t267; LC_7: CC45, t7061). While H_14 was susceptible to all tested antibiotic agents, LC_7 exhibited resistance to penicillin and ampicillin.

A selection of DNA microarray results is listed in Table 1 and full microarray results are provided as supplemental data (Supplement 3). Overall, strains from heifers and lactating herd mates exhibited highly similar prevalence rates of most resistance and virulence genes, whereas various statistically significant differences were detected when comparing these rates to the respective prevalences in the control strains. Amongst others, H and LC strains differed from C strains regarding the prevalence of various allelic variants of genes encoding adhesins, proteins involved in immunevasion, enterotoxins and enterotoxin-like superantigens, as well as genes involved in capsule and biofilm formation (Supplement 3).

Discussion

In the latex agglutination test, the vast majority of H and LC strains exhibited a SLAT(-) phenotype. The Staphaurex is a latex agglutination-based test used to confirm putative *Staph. aureus* isolates. In our study, *Staph. aureus* CC705 isolates could not be detected using the Staphaurex kit, which is consistent with recent findings (Stutz et al., 2011; Moser et al., 2013).

Risk factors and prevention strategies for heifer mastitis have been described in detail (Waage et al., 2001; Fox, 2009; Anderson et al., 2012), however, information on genomic characteristics of *Staph. aureus* from heifers is scarce and transmission of the organism

between heifers and lactating cows is controversially discussed (Roberson et al., 1994, Piepers et al., 2011, De Vliegher et al., 2012) In our study, characterization of *Staph. aureus* strains isolated from colostrum of heifers and milk of lactating herd mates yielded highly similar phenotypic and genotypic results not only for animals within the same herd, but across all tested herds. The strains were SLAT(-), belonged to *agr* type II, CC705 (former CC151), and *spa* type t529, and were susceptible to all antimicrobial agents. However, this homogeneous group differed significantly from strains isolated from mature cows in other herds (Moser et al., 2013). As the farms investigated in the study by Moser et al. and the farms in which we isolated *Staph. aureus* from heifer colostrum are spread throughout Switzerland, the high homogeneity among H and LC strains can not be attributed to close proximity of the respective farms. The closely related group of *Staph. aureus* detected in our study may possess a crucial competitive advantage needed for persistence within the udder of heifers throughout the first and potentially subsequent lactations. A SLAT(-) phenotype could favor persistence in the udder, as these strains are thought to be less virulent than SLAT(+) isolates and cause a weaker immune response (Zbinden et al., 2014). In addition, SLAT(-) strains are not recognized as *Staph. aureus* in routine diagnostic procedures as they yield false-negative results in the Staphaurex test and could therefore be misclassified as coagulase-negative *S. aureus.*

We conclude that strains isolated from colostrum of heifers and mastitis milk of lactating cows in the same herd feature highly similar phenotypic and genomic characteristics, suggesting either transmission between heifers and mature herd mates or persistence within the udder throughout the first and subsequent lactations. Further studies using high-resolution techniques such as the DNA microarray are needed to track a strain from the same cow over several lactations.

References

Anderson, K.L., R. Lyman, K. Moury, D. Ray, D.W. Watson, and M.T. Correa. 2012. Molecular epidemiology of *Staphylococcus aureus* mastitis in dairy heifers. J. Dairy Sci. 95:4921–4930.

CLSI. 2008. Performance standards for antimicrobial disk and dilution susceptibility tests for bacteria isolated from animals. 28. 3rd. ed. C. Wayne, PA.

Compton, C.W.R., C. Heuer, K. Parker, and S. McDougall. 2007. Risk factors for peripartum mastitis in pasture-grazed dairy heifers. J. Dairy Sci. 90:4171–4180.

Fox, L.K. 2009. Prevalence, incidence and risk factors of heifer mastitis. Vet. Microbiol. 134:82–88.

Moser, A., R. Stephan, S. Corti, and S. Johler. 2013. Comparison of genomic and antimicrobial resistance features of latex agglutination test-positive and latex agglutination test-negative *Staphylococcus aureus* isolates causing bovine mastitis. J. Dairy Sci. 96:329–334.

Piepers, S., G. Opsomer, H.W. Barkema, A. de Kruif, and S. De Vliegher. 2010. Heifers infected with coagulase-negative staphylococci in early lactation have fewer cases of clinical mastitis and higher milk production in their first lactation than noninfected heifers. J. Dairy Sci. 93:2014–2024.

Piepers, S., K. Peeters, G. Opsomer, H.W. Barkema, K. Frankena, and S. De Vliegher. 2011. Pathogen group specific risk factors at herd, heifer and quarter levels for intramammary infections in early lactating dairy heifers. Prev. Vet. Med. 99:91–101.

Pillar, C.M., L. Goby, D. Draghi, P. Grover, and C. Thornsberry. 2009. Evaluating the in vitro susceptibility of bovine mastitis pathogens to a combination of kanamycin and cefalexin: Recommendations for a disk diffusion test. J. Dairy Sci. 92:6217–6227.

Roberson, J.R., L.K. Fox, D.D. Hancock, C.C. Gay, and T.E. Besser. 1994. Coagulase-positive Staphylococcus intramammary infections in primiparous dairy cows. J. Dairy Sci. 77:958–969.

Shopsin, B., M. Gomez, S.O. Montgomery, D.H. Smith, M. Waddington, D.E. Dodge, D.A. Bost, M. Riehman, S. Naidich, and B.N. Kreiswirth. 1999. Evaluation of protein A gene polymorphic region DNA sequencing for typing of *Staphylococcus aureus* strains. J. Clin. Microbiol. 37:3556–3563.

Stutz, K., R. Stephan, and T. Tasara. 2011. SpA, ClfA, and FnbA genetic variations lead to Staphaurex test-negative phenotypes in bovine mastitis *Staphylococcus aureus* isolates. J. Clin. Microbiol. 49:638–646.

De Vliegher, S., L.K. Fox, S. Piepers, S. McDougall, and H.W. Barkema. 2012. Invited review: Mastitis in dairy heifers: nature of the disease, potential impact, prevention, and control. J. Dairy Sci. 95:1025–1040.

Waage, S., S. a Odegaard, a Lund, S. Brattgjerd, and T. Røthe. 2001. Case-control study of risk factors for clinical mastitis in postpartum dairy heifers. J. Dairy Sci. 84:392–399.

Wattinger, L., R. Stephan, F. Layer, and S. Johler. 2012. Comparison of *Staphylococcus aureus* isolates associated with food intoxication with isolates from human nasal carriers and human infections. Eur. J. Clin. Microbiol. Infect. Dis. 31:455–464.

Zbinden, C., R. Stephan, S. Johler, N. Borel, J. Bünter, R. M. Bruckmaier, and Ol. Wellnitz. The inflammatory response of primary bovine mammary epithelial cells to *Staphylococcus aureus* strains is linked to the bacterial phenotype. PLoS One 9: e87374.

Tables

Table 1: Comparison of prevalence rates of virulence and antibiotic resistance genes among *Staph. aureus* strains isolated from milk of heifers (H), lactating cows within the same herd (LC), and mature cows used as a control (C). Asterisks indicate statistically significant differences.

Group	Gene/Probe	Function	H (n = 32)	LC (n = 7)	C (n = 78)
Resistance[1]	*blaI/R/Z*	Beta Lactamase	0*[C]	14	13*[H]
	tetM	Tetracycline	0	14	0
Enterotoxins[2]	*sec*	Enterotoxin C	13	14	15
	ORF CM14	Enterotoxin-like Protein	97*[C]	86	53*[H]
	seg	Enterotoxin G	97*[C]	71	65*[H]
	sei	Enterotoxin I	97*[C]	100	65*[H]
	egc	Enterotoxin Gene Cluster	97*[C]	100	65*[H]
Virulence	*pvl*	Pantone-Valentine Leukocidin	0	0	0
	tst1	Toxic Shock Syndrome Toxin	13	0	8
	etA/B/C	Exfoliative Toxins	0	0	0
	aur	Aureolysin	100	86	97
	splE	Serine Protease E	3*[C]	0	35*[H]
	lukM/lukF-PV (P83)	Bovine Leukocidin	100*[C]	86	72*[H]

[1)] We did not detect the resistance genes *mecA, ermA/B/C, tetK, lnuA, msrA, mefA, mphC, vatA/B, vgaA/B, vanA/B/Z, fosB, aacA-aphD, aadD, aphA3, sat, dfrS1, far1, mupA, tetK, cat, fexA, cfr, qacA/C* among heifers and lactating cows within the same herd.

[2)] We did not detect the following genes encoding staphylococcal enterotoxins or enterotoxin-like superantigens in H or LC strains: *sea, seb, sed, see, seh, selj, selk, selq, selr.*

Acknowledgments

I would like to express my gratitude to the farmers that participated in this study. This project was partly funded by the Swiss Army.

Special thanks go to:

Prof. Roger Stephan, Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zürich, for giving me the opportunity to work on this scientific project, for his optimistic support and help when ever needed.

Dr. Sophia Johler, Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zürich, for her patience, for her help whenever necessary and for the preparation of the main review.

The whole ILS Team for their assistance and creation of a friendly working atmosphere.

All the other PhD and doctoral thesis students for the good times.

My parents Margrith and Werner Stalder-Häfliger for their care and appreciation.

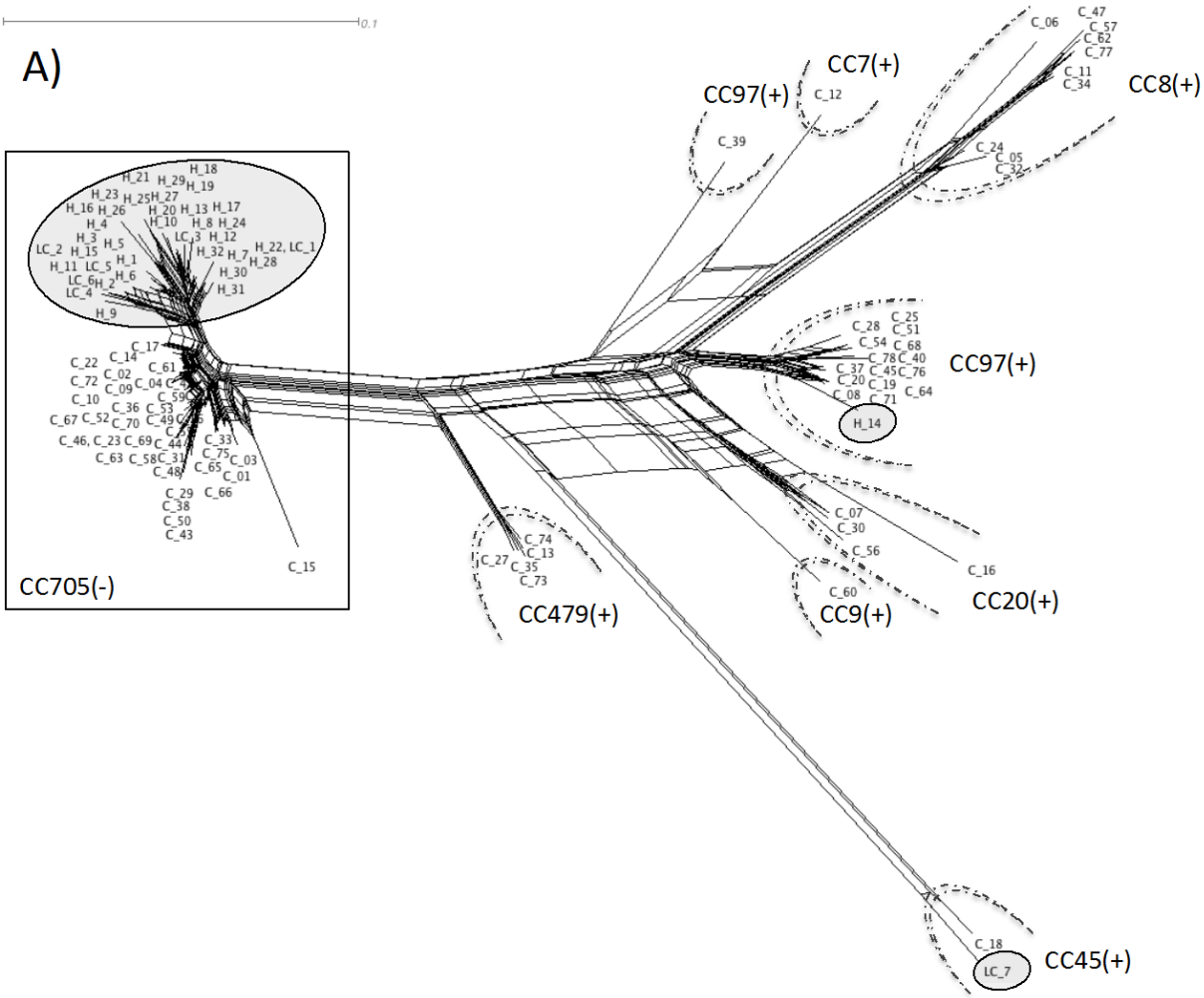
Barbara.

Supplemental data

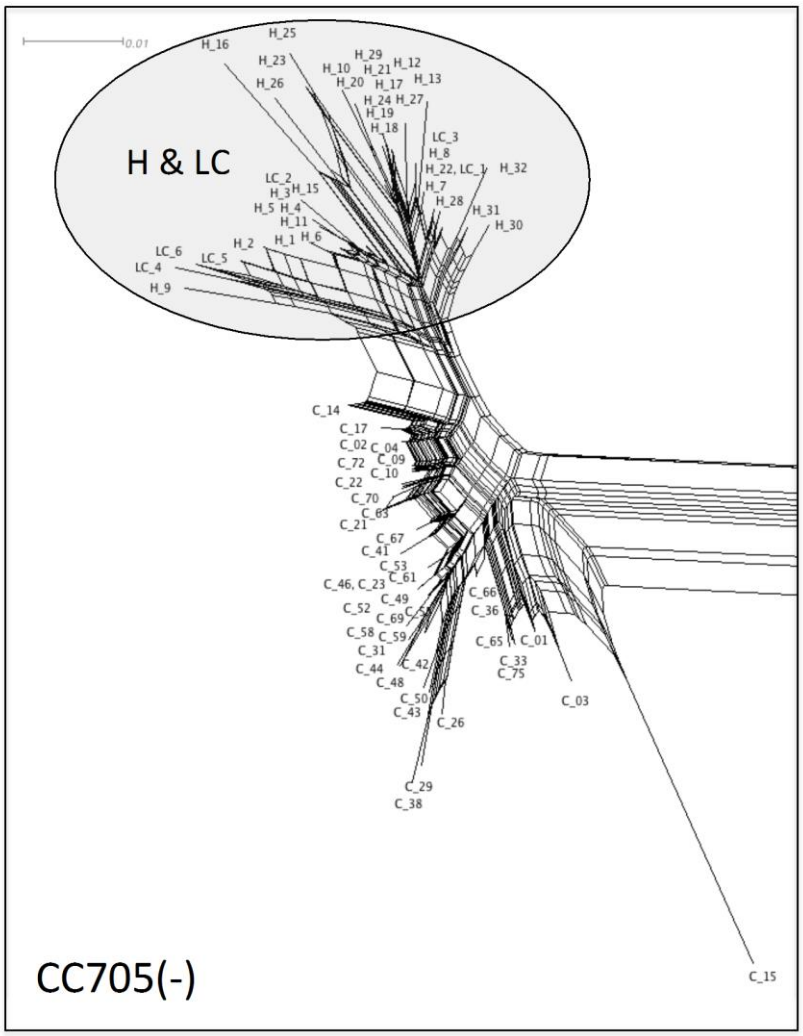
Supplement 1: Strains that were isolated more than once among the milk samples from heifers (H) and lactating cows in the same herd (LC).

ID	Farm	Source	Canton (regional district)
H_5	farm B	heifer	Thurgau
	farm A	heifer	Glarus
H_6	farm C	heifer	Bern
	farm A	heifer	Glarus
H_7	farm F	heifer	Graubünden
	farm G	heifer	Bern
H_8	farm D	heifer	Glarus
	farm A	heifer	Glarus
H_15	farm A	heifer	Glarus
	farm A	heifer	Glarus
	farm E	lactating cow (LC_2)	Appenzell Ausserrhoden
H_22	farm C	heifer	Appenzell Ausserrhoden
	farm A	heifer	Glarus
	farm C	lactating cow (LC_1)	Appenzell Ausserrhoden
LC_7	farm C	lactating cow	Bern
	farm C	lactating cow	Bern
	farm C	lactating cow	Bern

Supplement 2: SplitsTrees visualizing similarity of DNA microarray profiles of *Staph. aureus* isolated from milk samples of heifers (H), lactating cows within the same herd (LC), and mature cows serving as a control (C). *Staph. aureus* from heifers and lactating herd mates almost exclusively clustered into a highly homogeneous subgroup within CC705 (see circled areas). A) Overview over the full SplitsTree depicting all isolates and the assigned clonal complexes with SLAT phenotypes indicated in brackets. B) Detail view enlarging the SplitsTree region comprising only isolates that were assigned to CC705.



B)


0.01
H & LC
H_16
H_25
H_23
H_29
H_21
H_12
H_10
H_20
H_17
H_13
H_26
H_24
H_27
H_19
H_18
LC_3
H_8
H_22, LC_1
H_32
H_7
H_28
H_31
H_30
LC_2
H_3
H_15
H_5
H_4
H_11
H_2
H_1
H_6
LC_6
LC_5
LC_4
H_9
C_14
C_17
C_02
C_04
C_72
C_09
C_10
C_22
C_70
C_63
C_21
C_67
C_41
C_53
C_61
C_46, C_23
C_49
C_52
C_69
C_58
C_59
C_31
C_44
C_42
C_48
C_50
C_43
C_26
C_29
C_38
C_66
C_36
C_65
C_01
C_33
C_75
C_03
C_15
CC705(-)

Supplement 3: Prevalence of resistance and virulence genes among *Staph. aureus* isolated from colostrum of heifers (H), milk of lactating cows within the same herd (LC) and milk of mature cows used as a control (C).

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
Markers	rrnD1 (S. aureus)	Domain 1 of 23S-rRNA Gene	100	100	100			
	gapA	Glyceraldehyde 3-phosphate Dehydrogenase	100	100	100			
	katA	Catalase A	100	100	100			
	coA	Coagulase	100	100	100			
	spa	Staphylococcal Protein A	100	100	100			
	sbi	IgG-binding Protein	100	100	100			
	nuc1	Thermostable Extracellular Nuclease (DNAse)	100	100	100			
	fnbA (consensus)	Fibronectin-binding Protein A	100	100	95			
	vraS	vraS Sensor Protein	100	100	100			
	sarA	Staphylococcal Accessory Regulator A	100	100	100			
	eno	Enolase	100	100	100			
	saeS	Histidine Protein Kinase (sae Locus)	100	100	100			
Resistance	mecA	Methicillin, Oxacillin and all Beta-Lactams, defining MRSA	0	0	0			
	blaI	Beta Lactamase Repressor (Inhibitor)	0*^{C}	14	13*^{H}		0.033	
	blaR	Beta Lactamase Regulatory Protein	0*^{C}	14	13*^{H}		0.033	
	blaZ	Beta-Lactamase	0*^{C}	14	13*^{H}		0.033	
	erm(A)	Macrolide, Clindamycin	0	0	0			
	erm(B)	Macrolide, Clindamycin	0	0	0			
	erm(C)	Macrolide, Clindamycin	0	0	1			
	lnu(A)	Lincosamide	0	0	0			
	msr(A)	Macrolide	0	0	0			
	mef(A)	Macrolide	0	0	0			
	mph(C)	Macrolide	0	0	0			
	vat(A)	Virginiamycin A	0	0	0			
	vat(B)	Streptogramin A	0	0	0			
	vga(A)	Streptogramin A, Lincosamide, Pleuromutilin	0	0	0			
	vga(A) (BM 3327)	Streptogramin A (allele from BM 3327)	0	0	0			
	vgB(A)	Virginiamycin B, Pristinamycin	0	0	0			
	aacA-aphD	Aminoglycoside (Gentamicin, Tobramycin)	0	0	0			
	aadD	Aminoglycoside (Tobramycin)	0	0	0			
	aphA3	Aminoglycoside (Kanamycin, Neomycin)	0	0	0			
	sat	Streptothricin	0	0	0			
	dfrS1	Trimethoprim	0	0	0			
	far1	Fusidic acid	0	0	0			
	Q6GD50	Hypothetical Fusidic Acid Resistance Protein	0	0	0			
	mupA	Mupirocin	0	0	0			
	sdrM	Putative Transport Protein (=tetEfflux)	100	100	100			
	tet(K)	Tetracycline	0	0	0			
	tet(M)	Tetracycline	0	14	0			
	cat (consensus)	Chloramphenicol	0	0	0			
	fexA	Chloramphenicol, Florfenicol	0	0	0			
	cfr	Phenicols, Lincosamides, Oxazolidinones (Linezolid), Pleuromutilins, Streptogramin A	0	0	0			
	fosB	Metallothiol Transferase	0*^{C}	0	19*^{H}		0.005	

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
	vanA	Vancomycin	0	0	0			
	vanB	Vancomycin	0	0	1			
	vanZ	Vancomycin	0	0	0			
	qacA	Unspecific Efflux Pump	0	0	0			
	qacC (consensus)	Unspecific Efflux Pump	0	0	0			
Virulence	tst1 ("bovine" allele, from RF122)	Toxic Shock Syndrome Toxin, allele from bovine strains	13	0	8			
	tst1 (consensus)	Toxic Shock Syndrome Toxin	13	0	6			
	sea	Enterotoxin A	0	0	10			
	sea (320E)	Enterotoxin A, allele from 320E	0	0	9			
	sea (N315)	Enterotoxin A, allele from N315	0	0	1			
	seb	Enterotoxin B	0	0	0			
	sec	Enterotoxin C	13	14	15			
	ORF CM14	Enterotoxin-like Protein (ORF CM14)	96*^{C}	86	53*^{H}		0.000	
	sed	Enterotoxin D	0*C	0	12*^{H}			
	see	Enterotoxin E	0	0	0			
	seg	Enterotoxin G	97*^{C}	71	65*^{H}		0.001	
	seh	Enterotoxin H	0	0	0			
	sei	Enterotoxin I	97*^{C}	100	65*^{H}		0.001	
	sej	Enterotoxin J	0	0	8			
	sek	Enterotoxin K	0	0	0			
	sel	Enterotoxin L	13	14	15			
	selm	Enterotoxin-like Protein M	84*$^{LC, C}$	57*^{H}	64*^{H}	0.040	0.003	
	seln (consensus)	Enterotoxin-like Protein N	97*^{C}	100	65*^{H}		0.001	
	seln (other than RF122)	Enterotoxin-like Protein N (other than RF122)	38	14*^{C}	65*^{LC}			0.028
	selo	Enterotoxin-like Protein O	97*^{C}	100	65*^{H}		0.001	
	selu	Enterotoxin-like Protein U	97*^{C}	100	65*^{H}		0.001	
	seq	Enterotoxin Q	0	0	0			
	ser	Enterotoxin R	0	0	8			
	egc enterotoxin gene cluster	Enterotoxin Gene Cluster (*selm/seln/selo/selu*)	97*^{C}	100	65*^{H}		0.001	
	PVL	Pantone-Valentine Leukocidin	0	0	0			
	lukD	Leukocidin D Component	100	86	94			
	lukE	Leukocidin E Component	94	86	96			
	lukF	Haemolysin Gamma/Leukocidin, Component B (F)	100	100	100			
	lukM/lukF-PV (P83)	Bovine Leukocidin	100*^{C}	86	72*^{H}		0.001	
	lukS	Haemolysin Gamma/Leukocidin, Component C (S)	100	86	97			
	lukS (ST22+ST45)	Haemolysin Gamma/Leukocidin, Component C (S), allele from ST22/ST45	6	14	23			
	lukX	Leukocidin/Haemolysin Toxin Family Protein	100	100	100			
	lukY	Leukocidin/Haemolysin Toxin Family Protein	100	86	99			
	lukY (ST30+ST45)	Leukocidin/Haemolysin Toxin Family Protein, allele from ST22/ST45	0	14	3			
	hlgA	Haemolysin Gamma, Component A	100	100	99			
	hl	Putative Membrane Protein similar to Haemolysin	100	100	99			
	hla	Haemolysin Alpha (Alpha Toxin)	100	100	100			
	hlb	Haemolysine Beta (Phospholipase C)	100	86	99			
	hld	Haemolysin Delta (Amphiphylic Membrane Toxin)	100	100	100			
	hlIII (consensus)	Putative Haemolysin III	100	100	100			
	hlIII (other than RF122)	Putative Haemolysin III (other than RF122)	3*^{C}	0*^{C}	41*$^{H, LC}$		0.000	0.042
	un-disrupted hlb	Haemolysin Beta without Phage Insertion	88*^{LC}	43*$^{H, C}$	87*^{LC}	0.003		0.013
	sak	Staphylokinase	0*^{C}	14	13*^{H}		0.033	
	chp	Chemotaxis-inhibiting Protein (CHIPS)	0	14	1			

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
	scn	Staphylococcal Complement Inhibitor (SCIN)	0	14	12			
	etA	Exfoliative Toxin Serotype A	0	0	0			
	etB	Exfoliative Toxin Serotype B	0	0	0			
	etD	Exfoliative Toxin D	0	0	0			
	edinA	Epidermal Cell Differentiation Inhibitor A	0	0	0			
	edinB	Epidermal Cell Differentiation Inhibitor B	0	0	0			
	edinC	Epidermal Cell Differentiation Inhibitor C	0	0	0			
	aur (consensus)	Aureolysin	100	86	97			
	aur (MRSA252)	Aureolysin, allele from MRSA252	0	14	3			
	aur (other than MRSA252)	Aureolysin, allele from other than MRSA252	100	86	99			
	splA	Serine Protease A	97	86	90			
	splB	Serine Protease B	97	86	96			
	splE	Serine Protease E	3*C	0	35*H		0.001	
	sspA	Glutamylendopeptidase	100	100	99			
	sspB	Staphopain B, Protease	100	100	100			
	sspP	Staphopain A (Staphylopain A), Protease	100	100	100			
	ACME cluster	Arginine Catabolic Mobile Element	0	0	1			
	arcA-SCC	ACME-locus: Arginine Deiminase	0	0	0			
	arcB-SCC	ACME-locus: Ornithincarbamoyltransferase	0	0	0			
	arcC-SCC	ACME-locus: Carbamatkinase	0	0	0			
	arcD-SCC	ACME-locus: Arginine/Ornithine Antiporter	0	0	0			
agr-Typing	agrI (total)	Accessory Gene Regulator, Type 1	3*C	14	41*H		0.000	
	agrII (total)	Accessory Gene Regulator, Type 2	97*C	86	59*H		0.000	
	agrIII (total)	Accessory Gene Regulator, Type 3	0	0	0			
	agrIV (total)	Accessory Gene Regulator, Type 4	0	0	4			
SCCmec-Typing	mecA	Methicillin, Oxacillin and all Beta-Lactams, defining MRSA	0	0	0			
	mecI	Methicillin-Resistance Regulatory Protein	0	0	0			
	mecR	Signal Transducer Protein MecR1	0	0	0			
	ugpQ	Glycerophosphoryl-diester-Phosphodiesterase, associated with mecA	0	0	0			
	ccrA-1	Cassette Chromosome Recombinase A, type 1	0	0	0			
	ccrA-2	Cassette Chromosome Recombinase A, type 2	0*C	0	13*H		0.033	
	ccrA-3	Cassette Chromosome Recombinase A, type 3	0	0	0			
	ccrA-4	Cassette Chromosome Recombinase A, type 4	0	0	0			
	ccrAA (MRSAZH47)	Cassette Chromosome Recombinase A, type ZH47	0	0	1			
	ccrB-1	Cassette Chromosome Recombinase B, type 1	0	0	0			
	ccrB-2	Cassette Chromosome Recombinase B, type 2	0*C	0	13*H		0.033	
	ccrB-3	Cassette Chromosome Recombinase B, type 3	0	0	0			
	ccrB-4	Cassette Chromosome Recombinase B, type 4	0	0	0			
	ccrC (85-2082)	Cassette Chromosome Recombinase C	0	0	0			
	merA	Mercury Resistance Operon, Hg(II) Reductase	0	0	0			
	merB	Mercury Resistance Operon, Alkylmercury Lyase	0	0	0			
	kdpA-SCC	Potassium-transporting ATPase A, chain 2	0	0	0			
	kdpB-SCC	Potassium-transporting ATPase B, chain 1	0	0	0			
	kdpC-SCC	Potassium-transporting ATPase C, chain 2	0	0	0			
	kdpD-SCC	Sensor Histidine Kinase (Sensor Protein located in kdp operon)	0	0	0			
	kdpE-SCC	KDP Operon Transcriptional Regulatory Protein (DNA-binding Response Regulator)	0	0	0			
	plsSCC (COL)	Plasmin-sensitive Surface Protein	0	0	0			
	Q9XB68-dcs	Hypothetical Protein Historical Name: CN050 Synonyms: dcs	0	0	0			
	xylR	Homolog of Xylose Repressor, associated with SCCmec-elements	0	0	0			

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
Capsule/Biofilm	cap1 (total)	Capsule Type 1	0	0	0			
	cap5 (total)	Capsule Type 5	3*[C]	0*[C]	38*[H, LC]		0.000	0.048
	cap8 (total)	Capsule Type 8	97*[C]	100*[C]	62*[H, LC]		0.000	0.048
	capH1	Capsular Polysaccharide Synthesis Enzyme CapH Capsule Type 1	0	0	0			
	capJ1	O-Antigen Polymerase CapJ Capsule Type 1	0	0	0			
	capK1	Capsular Polysaccharide Biosynthesis Protein CapK Capsule Type 1	0	0	0			
	capH5	Capsular Polysaccharide Synthesis Enzyme CapH Capsule Type 5	3*[C]	0*[C]	38*[H, LC]		0.000	0.048
	capJ5	O-Antigen Polymerase CapJ Capsule Type 5	3*[C]	0*[C]	38*[H, LC]		0.000	0.048
	capK5	Capsular Polysaccharide Biosynthesis Protein CapK Capsule Type 5	3*[C]	0*[C]	38*[H, LC]		0.000	0.048
	capH8	Capsular Polysaccharide Synthesis Enzyme CapH Capsule Type 8	97*[C]	100*[C]	62*[H, LC]		0.000	0.048
	capI8	Capsular Polysaccharide Synthesis Enzyme CapI Capsule Type 8	97*[C]	100*[C]	62*[H, LC]		0.000	0.048
	capJ8	O-Antigen Polymerase CapJ Capsule Type 8	97*[C]	100*[C]	62*[H, LC]		0.000	0.048
	capK8	Capsular Polysaccharide Biosynthesis Protein CapK Capsule Type 8	97*[C]	100*[C]	62*[H, LC]		0.000	0.048
	icaA	Intercellular Adhesion Protein A (N-glycosyltransferase)	100	100	99			
	icaC	Intercellular Adhesion Protein C	100	100	99			
	icaD	Biofilm PIA Synthesis Protein D	100	100	99			
	bap	Surface Protein Involved in Biofilm Formation	0	0	0			
MSCRAMMs/Adhesion	bbp (consensus)	Bone Sialoprotein-Binding Protein	94	100	94			
	bbp (COL+MW2)	Bone Sialoprotein-Binding Protein, allele from COL/MW2	0	0	12			
	bbp (MRSA252)	Bone Sialoprotein-Binding Protein, allele from MRSA252	0	0	1			
	bbp (Mu50)	Bone Sialoprotein-Binding Protein, allele from Mu50	3*[C]	0	22*[H]		0.016	
	bbp (RF122)	Bone Sialoprotein-Binding Protein, allele from RF122	91*[C]	86	51*[H]		0.000	
	bbp (ST45)	Bone Sialoprotein-Binding Protein, allele from ST45	0	14	1			
	clfA (consensus)	Clumping Factor A	100	100	99			
	clfA (COL+RF122)	Clumping Factor A, allele from COL/RF122	91*[C]	86	86*[H]		0.033	
	clfA (MRSA252)	Clumping Factor A, allele from MRSA252	0*[C]	0*[C]	55*[H, LC]		0.000	0.002
	clfA (Mu50+MW2)	Clumping Factor A, allele from Mu50/MW2	9*[C]	14*[C]	99*[H, LC]		0.049	0.001
	clfB (consensus)	Clumping Factor B	100	100	100			
	clfB (COL+Mu50)	Clumping Factor B, allele from COL/Mu50	0*[C]	0	13*[H]		0.033	
	clfB (MW2)	Clumping Factor B, allele from MW2	0	14	54			
	clfB (RF122)	Clumping Factor B, allele from RF122	97*[C]	86	60*[H]		0.000	
	cna	Collagen-Binding Adhesin	0	14	9			
	ebh (consensus)	Cell Wall Associated Fibronectin-Binding Protein	100	100	99			
	eno	Enolase	100	100	100			
	fib	Fibrinogen Binding Protein	100	86	99			
	fib (MRSA252)	Fibrinogen Binding Protein, allele from MRSA252	0	0	3			
	ebpS	Cell Surface Elastin Binding Protein	100	100	99			
	ebpS (01-1111)	Cell Surface Elastin Binding Protein, allele from ST45	0	14	3			
	ebpS (COL)	Cell Surface Elastin Binding Protein, allele from COL	0*[C]	0	19*[H]		0.005	
	fnbA (consensus)	Fibronectin-Binding Protein A	100	100	95			
	fnbA (COL)	Fibronectin-Binding Protein A, allele from COL	0*[C]	0	14*[H]		0.032	
	fnbA (MRSA252)	Fibronectin-Binding Protein A, allele from MRSA252	0	0	8			
	fnbA (Mu50+MW2)	Fibronectin-Binding Protein A, allele from Mu50/MW2	0	14	1			
	fnbA (RF122)	Fibronectin-Binding Protein A, allele from RF122	97*[C]	86	51*[H]		0.000	
	fnbB (COL)	Fibronectin-Binding Protein B, allele from COL	0*[C]	0	13*[H]		0.033	
	fnbB (COL+Mu50+MW2)	Fibronectin-Binding Protein B, allele from COL/Mu50/MW2	3*[C]	14	49*[H]		0.000	
	fnbB (Mu50)	Fibronectin-Binding Protein B, allele from Mu50	0*[C]	0	33*[H]		0.000	

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
	fnbB (MW2)	Fibronectin-Binding Protein B, allele from MW2	0	0	0			
	fnbB (ST15)	Fibronectin-Binding Protein B, allele from ST15	0	0	5			
	fnbB (ST45-2)	Fibronectin-Binding Protein B, allele from ST45	0	0	1			
	map (consensus)	Major Histocompatibility Complex Class II Analog Protein	97	100	100			
	map (COL)	Major Histocompatibility Complex Class II Analog Protein, allele from COL	97	86	94			
	map (MRSA252)	Major Histocompatibility Complex Class II Analog Protein, allele from MRSA252	0	14	1			
	map (Mu50+MW2)	Major Histocompatibility Complex Class II Analog Protein, allele from Mu50/MW2	6*C	0*C	65*H, LC		0.000	0.001
	sdrC (consensus)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C	97	100	100			
	sdrC (B1)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C, allele from B1	0	14	1			
	sdrC (COL)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C, allele from COL	0*C	0	21*H		0.005	
	sdrC (Mu50)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C, allele from Mu50	3*C	0	27*H		0.005	
	sdrC (MW2+MRSA252+RF122)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C, allele from MW2/MRSA252/RF122	91*C	86	68*H		0.010	
	sdrC (other than MRSA252+RF122)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein C, allele from other than MRSA252/RF122	3*C	0*C	41*H, LC		0.000	0.042
	sdrD (COL+MW2)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein D, allele from COL/MW2	0*C	14	14*H		0.032	
	sdrD (consensus)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein D	3*C	14	37*H		0.000	
	sdrD (Mu50)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein D, allele from Mu50	3*C	0	21*H		0.021	
	sdrD (other)	Ser-Asp Rich Fibrinogen-Binding, Bone Sialoprotein-Binding Protein D, allele from other than COL/MW2/MRSA252	0	0	3			
	vwb (consensus)	van Willebrand Factor - Binding Protein	100	100	99			
	vwb (COL+MW2)	van Willebrand Factor - Binding Protein, allele from COL/MW2	0*C	0	13*H		0.033	
	vwb (MRSA252)	van Willebrand Factor - Binding Protein, allele from MRSA252	0	14	3			
	vwb (Mu50)	van Willebrand Factor - Binding Protein, allele from Mu50	0	0	5			
	vwb (RF122)	van Willebrand Factor - Binding Protein, allele from RF122	100*C	86	72*H		0.001	
	sasG (consensus)	Staphylococcus aureus Surface Protein G	3*C	0*C	45*H, LC		0.000	0.038
	sasG (COL+Mu50)	Staphylococcus aureus Surface Protein G, allele from COL/Mu50	3*C	0*C	45*H, LC		0.000	0.038
	sasG (MW2)	Staphylococcus aureus Surface Protein G, allele from MW2	0	0	0			
	sasG (other than MRSA252+RF122)	Staphylococcus aureus Surface Protein G, allele from other than MRSA252/RF122	3*C	0*C	45*H, LC		0.000	0.038
Immunevasion/Misc.	isaB	Immunodominant Antigen B	100	86	100			
	isaB (MRSA252)	Immunodominant Antigen B, allele from MRSA252	0	14	100			
	mprF (COL+MW2)	Lysylphosphatidylglycerol Synthetase (Defensin Resistance), allele from COL/MW2	100	86	92			
	mprF (Mu50+MRSA252)	Lysylphosphatidylglycerol Synthetase (Defensin Resistance), allele from Mu50/MRSA252	0*C	0	9*H		0.043	
	isdA (consensus)	Transferrin-Binding Protein	100	100	99			
	isdA (MRSA252)	Transferrin-Binding Protein, allele from MRSA252	0	14	3			
	isdA (other than MRSA252)	Transferrin-Binding Protein, allele from other than MRSA252	100	86	97			
	Imrp	Hypothetical Transporter Protein	3*C	14*C	100*H, LC		0.000	0.000
	ImrP (RF122	Hypothetical Transporter Protein, allele from RF122	97*C	86	59*H		0.000	
	Q2YUB3	Multidrug Resistance Protein	100*C	86	82*H		0.009	
	hsdS1 (RF122)	Site-specific Deoxyribonuclease Subunit Type 1, allele from RF122	97*C	86	51*H		0.000	
	hsdS2 (MRSA252)	Site-specific Deoxyribonuclease Subunit Type 2, allele from MRSA252	0	14	3			
	hsdS2 (Mu50+N315+COL+USA300+NCTC8325)	Site-specific Deoxyribonuclease Subunit Type 2, allele from Mu50/N315/COL/USA300/NCTC8325	0*C	0	21*H		0.006	
	hsdS2 (MW2+MSSA476)	Site-specific Deoxyribonuclease Subunit Type 2, allele from MW2/MRSA476	0*C	0*C	37*H, LC		0.000	0.038
	hsdS2 (RF122)	Site-specific Deoxyribonuclease Subunit Type 1, allele from RF122	97*C	86	50*H		0.000	
	hsdS3 (all other than RF122+ MRSA252)	Site-specific Deoxyribonuclease Subunit Type 3, allele from any other than MRSA252 / RF122	69	43	64			
	hsdS3 (CC51+ MRSA252)	Site-specific Deoxyribonuclease Subunit Type 3, allele from CC51/MRSA252	0	0	0			
	hsdS3 (COL+USA300+NCTC8325+MW2 +MSSA476+RF122)	Site-specific Deoxyribonuclease Subunit Type 3, allele from COL/USA300/NCTC8325/MW2/MSSA476/RF122	97*C	86	71*H		0.002	
	hsdS3 (MRSA252)	Site-specific Deoxyribonuclease Subunit Type 3, allele from MRSA252	0	0	0			
	hsdS3 (Mu50+N315)	Site-specific Deoxyribonuclease Subunit Type 3, allele from Mu50/N315	0	0	1			
	hsdSx (CC15)	Site-specific Deoxyribonuclease Subunit Type X, allele from CC15	0	0	1			

Group	Gene/Probe	Function	Prevalence (%) H (n = 32)	LC (n = 7)	C (n = 78)	P value HxLC	HxC	LCxC
	hsdSx (CC25)	Site-specific Deoxyribonuclease Subunit Type X, allele from CC25	100*C	86	85*H		0.017	
	hsdSx (etd)	Site-specific Deoxyribonuclease Subunit Type X, allele from etd	0	0	1		1.000	
	Q2FXC0	Hypothetical Protein, next to Serine Protease Operon	0*C	0	13*H		0.033	
	Q7A4X2	Hypothetical Protein, next to entG	100*C	100	86*H		0.032	
	hysA1 (MRSA252)	Hyaluronate Lyase A1, MRSA252	0	0	0			
	hysA1 (MRSA252+RF122) and/or hysA2 (COL+USA300)	Hyalunorate Lyase A1, alleles from MRSA252/RF122 and Hyalunorate LyaseA2, alleles from COL/USA300	97*C	86	64*H		0.000	
	hysA1 (MRSA252+RF122) and/or hysA2 (consensus)	Hyalunorate Lyase A1, alleles from MRSA252/RF122 and Hyalunorate Lyase A2, all alleles	100	100	100			
	hysA2 (all other than COL+USA300+NCTC8325)_probe1	Hyaluronate Lyase A2, any other allele than COL/USA300 /NCTC8325	100*C	86	86*H		0.032	
	hysA2 (all other than MRSA252)	Hyaluronate Lyase A2, any other allele than MRSA252	97*C	86	64*H		0.000	
	hysA2 (COL+USA300+NCTC8325)	Hyaluronate Lyase A2, COL/USA300/NCTC8325	97*C	86	64*H		0.000	
	hysA2 (MRSA252)	Hyaluronate Lyase A2, MRSA252	0	0	0			
set/sel Genes	setB1	Staphylococcal Superantigen-like Protein B1	97	57	99			
	setB2	Staphylococcal Superantigen-like Protein B2	100	86	99			
	setB2 (MRSA252)	Staphylococcal Superantigen-like Protein B2, allele from MRSA252	0	0	0			
	setB3	Staphylococcal Superantigen-like Protein B3	100	86	99			
	setB3 (MRSA252)	Staphylococcal Superantigen-like Protein B3, allele from MRSA252	0	14	1			
	setC/selx	Staphylococcal Superantigen-like Protein C/SAg Gene Homolog, SAUSA300_0370	100	86	99			
	ssl01/set6 (COL)	Staphylococcal Superantigen-like Protein 1, allele from COL	0	0	8			
	ssl01/set6 (MRSA252)	Staphylococcal Superantigen-like Protein 1, allele from MRSA252	0	0	1			
	ssl01/set6 (Mu50+N315)	Staphylococcal Superantigen-like Protein 1, allele from Mu50/N315	0*C	0	13*H		0.033	
	ssl01/set6 (MW2+MSSA476)	Staphylococcal Superantigen-like Protein 1, allele from MW2/MSSA476	0	0	9			
	ssl01/set6 (other alleles)	Staphylococcal Superantigen-like Protein 1, all other alleles	0*C	0*C	81*H, LC		0.000	0.000
	ssl01/set6 (RF122)	Staphylococcal Superantigen-like Protein 1, allele from RF122	97*C	86	78*H		0.036	
	ssl02/set7	Staphylococcal Superantigen-like Protein 2	100	86	100			
	ssl03/set8	Staphylococcal Superantigen-like Protein 3	97	86	92			
	ssl03/set8 (MRSA252, SAR0424)	Staphylococcal Superantigen-like Protein 3, allele from MRSA252/SAR0424	0	0	0			
	ssl04/set9	Staphylococcal Superantigen-like Protein 4	3*C	0*C	46*H, LC		0.000	0.019
	ssl04/set9 (MRSA252, SAR0425)	Staphylococcal Superantigen-like Protein 4, allele from MRSA252/SAR0425	0	14	5			
	ssl05/set3	Staphylococcal Superantigen-like Protein 5	6*C	0*C	94*H, LC		0.000	0.000
	ssl05/set3 (MRSA252)	Staphylococcal Superantigen-like Protein 5, allele from MRSA252	0	14	1			
	ssl05/set3 (RF122, probe-611)	Staphylococcal Superantigen-like Protein 4, allele from RF122	97*C	86	82*H		0.031	
	ssl06 (NCTC8325+MW2)	Staphylococcal Superantigen-like Protein 6, allele from NCTC8325/MW2	0*C	0	21*H		0.005	
	ssl06/set21	Staphylococcal Superantigen-like Protein 6	0*C	0	21*H		0.005	
	ssl07/set1	Staphylococcal Superantigen-like Protein 7	100	86	99			
	ssl07/set1 (AF188836)	Staphylococcal Superantigen-like Protein 7, allele from AF188836	0	14	1			
	ssl07/set1 (MRSA252)	Staphylococcal Superantigen-like Protein 7, allele from MRSA252	0	0	5			
	ssl08/set12	Staphylococcal Superantigen-like Protein 8	100*LC	43*H, LC	97*LC	0.015		0.017
	ssl09/set5	Staphylococcal Superantigen-like Protein 9	97	86	95			
	ssl09/set5 (MRSA252)	Staphylococcal Superantigen-like Protein 9, allele from MRSA252	0	14	1			
	ssl10 (RF122)	Staphylococcal Superantigen-like Protein 10, allele from RF 122	97*C	86	58*H		0.000	
	ssl10/set4	Staphylococcal Superantigen-like Protein 10	3*C	0*C	73*H, LC		0.000	0.007
	ssl10/set4 (MRSA252)	Staphylococcal Superantigen-like Protein 10, allele from MRSA252	0	14	9			
	ssl11/set2 (COL)	Staphylococcal Superantigen-like Protein 11, allele from COL	0*C	0	13*H		0.033	
	ssl11/set2 (MRSA252)	Staphylococcal Superantigen-like Protein 11, allele from MRSA252	0	0	0			
	ssl11+set2 (Mu50+N315)	Staphylococcal Superantigen-like Protein 11, allele from Mu50/N315	0	0	0			
	ssl11+set2 (MW2+MSSA476)	Staphylococcal Superantigen-like Protein 11, allele from MW2/MSSA476	97*C	86	51*H		0.000	

Curriculum Vitae

Vorname Name	Ueli Stalder
Geburtsdatum	24/07/1987
Geburtsort	Wolhusen LU
Nationalität	Schweizer
Heimatort	Schüpfheim LU

08/1994 – 07/2000	Primarschule, Oberberg Schüpfheim, Schweiz
08/2000 – 07/2007	Kantonsschule, Schüpfheim, Schweiz
19/06/2007	Erlangung der Maturität an der Kantonsschule Schüpfheim, Schwerpunkt Latein
09/2007 – 01/2013	Studium der Veterinärmedizin an der Vetsuisse-Fakultät Universität Bern, Schweiz
23/01/2013	Erlangung des Diploms für Tierärzte an der Vetsuisse-Fakultät Universität Bern, Schweiz
06/2013 – 04/2014	Anfertigung der Dissertation unter der Leitung von Prof. Dr. Roger Stephan am Institut für Lebensmittelsicherheit und –hygiene der Vetsuisse-Fakultät Universität Zürich Direktor: Prof. Dr. Roger Stephan